Validated By CRFValidator v 1.0.3

Application No: 10580901 Version No: 3.0

Input Set:

Output Set:

Started: 2007-09-12 16:33:57.345
Finished: 2007-09-12 16:33:58.037
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 692 ms
Total Warnings: 11
Total Errors: 0
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code		Error Description
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W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
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W	213	Artificial or Unknown found in <213> in SEQ ID (11)

SEQUENCE LISTING

<110> Mridula, Sharma
Berry, Carole
Thomas, Mark
Kambadur, Ravi
Bower, Robert Syndecombe

<120> Novel Muscle Growth Regulator

<130> AJPARK39.001APC

<140> 10580901
<141> 2007-09-12

<150> PCT/NZ2004/000308
<151> 2004-11-26

<150> NZ529860
<151> 2003-11-28

<160> 11

<170> PatentIn version 3.1

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<212> DNA
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ccggacgccg aaccgccgcc gctgcttcag acgcagaccc caccgccgac tctgcagcag 180

cccgccccgc ccggcagcga gcggcgcctt ccaactccgg agcaaatttt tcagaacata 240

aaacaagaat atagtcgtta tcagaggtgg agacatttag aagttgttct taatcagagt 300

gaagcttgta cttcggaaag tcagcctcac tcctcagcac tcacagcacc tagttctcca 360

ggttcctcct ggatgaaaaa ggaccagccc acctttaccc tccgacaagt tggaataata 420

tgtgagcgtc tcttaaaaga ctatgaagat aaaattcggg aggaatatga gcaaatcctc 480

aatactaaac tagcagaaca atatgaatct tttgtgaaat tcacacatga tcagattatg 540

cgacgatatg ggacaaggcc aacaagctat gtatcc 576

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20 25 30

Gly Pro Thr Pro Gly Leu Arg Pro Pro Asp Ala Glu Pro Pro Pro Leu
35 40 45

Leu Gln Thr Gln Thr Pro Pro Pro Thr Leu Gln Gln Pro Ala Pro Pro
50 55 60

Gly Ser Glu Arg Arg Leu Pro Thr Pro Glu Gln Ile Phe Gln Asn Ile
65 70 75 80

Lys Gln Glu Tyr Ser Arg Tyr Gln Arg Trp Arg His Leu Glu Val Val
85 90 95

Leu Asn Gln Ser Glu Ala Cys Thr Ser Glu Ser Gln Pro His Ser Ser
100 105 110

Ala Leu Thr Ala Pro Ser Ser Pro Gly Ser Ser Trp Met Lys Lys Asp
115 120 125

Gln Pro Thr Phe Thr Leu Arg Gln Val Gly Ile Ile Cys Glu Arg Leu
130 135 140

Leu Lys Asp Tyr Glu Asp Lys Ile Arg Glu Glu Tyr Glu Gln Ile Leu
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Asn Thr Lys Leu Ala Glu Gln Tyr Glu Ser Phe Val Lys Phe Thr His
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Asp Gln Ile Met Arg Arg Tyr Gly Thr Arg Pro Thr Ser Tyr Val Ser
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cccgccccgc ccggcagcga ccggcgcctt ccaactccgg agcaaatttt tcagaacata 240

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gaagcttgta cttcggaaag tcagcctcac tcctcaacac tcacagcacc tagttctcca 360

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Gly Pro Thr Pro Gly Leu Arg Pro Pro Asp Ala Glu Pro Pro Pro Leu
35 40 45

Leu Gln Thr Gln Ile Pro Pro Pro Thr Leu Gln Gln Pro Ala Pro Pro
50 55 60

Gly Ser Asp Arg Arg Leu Pro Thr Pro Glu Gln Ile Phe Gln Asn Ile
65 70 75 80

Lys Gln Glu Tyr Ser Arg Tyr Gln Arg Trp Arg His Leu Glu Val Val
85 90 95

Leu Asn Gln Ser Glu Ala Cys Thr Ser Glu Ser Gln Pro His Ser Ser
100 105 110

Thr Leu Thr Ala Pro Ser Ser Pro Gly Ser Ser Trp Met Lys Lys Asp
115 120 125

Gln Pro Thr Phe Thr Leu Arg Gln Val Gly Ile Ile Cys Glu Arg Leu
130 135 140

Leu Lys Asp Tyr Glu Asp Lys Ile Arg Glu Glu Tyr Glu Gln Ile Leu
145 150 155 160

Asn Thr Lys Leu Ala Glu Gln Tyr Glu Ser Phe Val Lys Phe Thr His
165 170 175

Asp Gln Ile Met Arg Arg Tyr Gly Thr Arg Pro Thr Ser Tyr Val Ser
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taaaacacta atattccaag gcacactcaa tgttttaaag gatcacagag tgactaccaa 180

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